

Sequence Comparison C

RESULT 1
 JN0621
 G protein-coupled receptor type B - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
 C;Accession: JN0621
 R;Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
 Biochem. Biophys. Res. Commun. 194, 504-511, 1993
 A;Title: Identification of novel members of G-protein coupled receptor superfamily
 expressed in bovine taste tissue.
 A;Reference number: JN0621; MUID:93326166
 A;Accession: JN0621
 A;Molecule type: mRNA
 A;Residues: 1-350 <MAT>
 A;Cross-references: GB:S63848; NID:g399710; PIDN:AAB27547.1; PID:g399711
 A;Experimental source: tongue taste papillae
 C;Comment: This protein is involved in modulating taste sensitivity or regeneration of
 taste cells.
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
 F;42-66/Domain: transmembrane #status predicted <TM1>
 F;80-99/Domain: transmembrane #status predicted <TM2>
 F;114-135/Domain: transmembrane #status predicted <TM3>
 F;154-175/Domain: transmembrane #status predicted <TM4>
 F;200-222/Domain: transmembrane #status predicted <TM5>
 F;242-265/Domain: transmembrane #status predicted <TM6>
 F;284-306/Domain: transmembrane #status predicted <TM7>
 F;6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.1%; Score 1620; DB 2; Length 350;
 Best Local Similarity 86.0%; Pred. No. 1.1e-131;
 Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

Qy	1	MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS	60
Db	1	MAVEYNQSTDYYYEENEMNDTHDYSQYEVICIKKEVRKFAKVFLPAFFTIAFIIGLAGNS	60
Qy	61	MVVAIYAYYKKQRTKTDVYIILNLAVADLLLLFTLPFWAVNAVHGWLKGKIMCKITSALYT	120
Db	61	TVVAIYAYYKKRRTKTDVYIILNLAVADLFLFTLPFWAVNAVHGWLKGKIMCKVTSALYT	120
Qy	121	LNFSVGMQFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVWMAAILLSIPQLVFYTVND	180
Db	121	VNFSVGMQFLACISTDRYWAVTKAPSQSGVGKPCWVICFCVWVAAILLSIPQLVFYTVNH	180
Qy	181	NARCIPIFPYRLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK	240
Db	181	KARCVPIFPYHLGTSMKASIQILEICIGFIIPFLIMAVCYFITAKTLIKMPNIKKSQPLK	240
Qy	241	VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNP	300
Db	241	VLFTVVIVFIVTQLPYNIVKFCQAIIDIIYSLITDCMSKRMDVAIQITESIALFHSCLNP	300
Qy	301	ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPDSEGPTEPTSTFSI	350
Db	301	VLYVFMGTSFKNYIMKVAKKYGSWRRQRQNVVEEIPFESEDATEPTSTFSI	350